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OM protein - protein search, using sw model

Run on: February 13, 2002, 10:09:12 ; Search time 10.31 Seconds
(without alignments)
67.569 Million cell updates/sec

Title: US-09-486-094-12

Perfect score: 51

Sequence: 1 XCXXXXXXCXXXXX 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	54.9	58	MT2_CALSI	P55950 callinectes
2	28	54.9	59	MT1_CALSI	P55949 callinectes
3	27	52.9	58	MT1_SCYSE	P02805 scylla serr
4	27	52.9	572	NH25_CAEEL	Q19345 caenorhabdi
5	27	52.9	4543	LRP1_CHICK	P98157 gallus gall
6	27	52.9	4544	LRP1_HUMAN	Q07954 homo sapien
7	26	51.0	57	MT2_SCYSE	P02806 scylla serr
8	26	51.0	58	MT1_HOMAM	P29499 homarus ame
9	26	51.0	58	MT1_ASTFL	P55951 astacus flu
10	26	51.0	58	MT_CARMA	P55948 carcinus ma
11	26	51.0	58	MT_POTPO	P55952 potamon pot
12	26	51.0	67	THB1_THETS	P82354 theromyzon
13	26	51.0	455	TNR1_HUMAN	P19438 homo sapien
14	26	51.0	493	FBL3_HUMAN	Q12805 homo sapien
15	26	51.0	493	FBL3_RAT	Q35568 rattus norv
16	26	51.0	721	PRTP_HSV7J	P52385 human herpe
17	26	51.0	1046	PSTA_DICDI	P11976 dictyostelli
18	26	51.0	1246	YMW2_CAEEL	P34504 caenorhabdi
19	26	51.0	1253	POLS_SFV	P03315 semliki for
20	26	51.0	1390	INSR_AEDAE	Q93105 aedes aegyp
21	26	51.0	2139	CRB_DROME	P10040 drosophila
22	26	51.0	4753	LRP_CAEEL	Q04833 caenorhabdi
23	25	49.0	71	MT21_MYTED	P80251 mytilus edu
24	25	49.0	71	MT22_MYTED	P80252 mytilus edu
25	25	49.0	71	MT23_MYTED	P80253 mytilus edu
26	25	49.0	71	NKL2_NAJME	P01388 naja melano
27	25	49.0	72	MT13_MYTED	P80248 mytilus edu
28	25	49.0	78	MT2_ACTCH	P43390 actinidia c
29	25	49.0	117	WAP_CAMDR	P09837 camelus dro
30	25	49.0	132	WAP_PIG	O46655 sus scrofa
31	25	49.0	151	KR2C_SHEEP	P02440 ovis aries
32	25	49.0	194	KRUB_HUMAN	O75690 homo sapien
33	25	49.0	201	ADEN_ADE04	P07885 human adeno

34	25	49.0	328	1	LIPB_YEAST	Q06005 saccharomyc
35	25	49.0	410	1	PRTP_HSV6Z	P52544 human herpe
36	25	49.0	448	1	FBL5_HUMAN	Q9ubx5 homo sapien
37	25	49.0	540	1	GUX1_ASPAC	O59843 aspergillus
38	25	49.0	575	1	TRBM_HUMAN	P07204 homo sapien
39	25	49.0	726	1	PRTP_HSV6U	P52384 human herpe
40	25	49.0	790	1	AD30_HUMAN	Q9ukf2 homo sapien
41	25	49.0	1254	1	POLS_RRVN	P13890 ross river
42	25	49.0	1254	1	POLS_RRVN	P08491 ross river
43	25	49.0	4655	1	LRP2_HUMAN	P08164 homo sapien
44	24	47.1	61	1	MT1_CRIGR	P02804 cricetus
45	24	47.1	61	1	MT1_YEAST	P07215 saccharomyc

ALIGNMENTS

RESULT 1
ID MT2_CALSI STANDARD; PRT; 58 AA.
AC P55950;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN-II (MT-II) (MT-IIB/MT-IIA).
OS Callinectes sapidus (Blue crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Callinectes.
OX NCBI_TaxID=6763;
RN [1]
RP SEQUENCE.
RX MEDLINE=96033062; PubMed=7487904;
RA Brouwer M., Enghild J., Hoexum-Brouwer T., Thøgersen I., Truncali A.;
RT "Primary structure and tissue-specific expression of blue crab
(Callinectes sapidus) metallothionein isoforms.";
RL Biochem.J. 311:617-622(1995).
CC -!- FUNCTION: BINDS SIX DIVALENT METAL IONS. KNOWN TO BIND COPPER AND
CADMIUM.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR HSSP; P55949; 1DMD.
DR InterPro; IPR003019; Metallothion.
DR InterPro; IPR002045; Metallothion_crust.
DR Pfam; PF00131; metalthio; 1.
DR PRINTS; PR00858; MTCRUSTACEAN.
KW Metal-binding; Metal-thiolate cluster; Chelation; Copper; Cadmium.
FT DOMAIN 1 29 BETA.
FT DOMAIN 30 58 ALPHA.
FT METAL 5 5 CLUSTER B.
FT METAL 6 6 CLUSTER B.
FT METAL 10 10 CLUSTER B.
FT METAL 12 12 CLUSTER B.
FT METAL 17 17 CLUSTER B.
FT METAL 21 21 CLUSTER B.
FT METAL 23 23 CLUSTER B.
FT METAL 26 26 CLUSTER B.
FT METAL 28 28 CLUSTER B.
FT METAL 31 31 CLUSTER A.
FT METAL 34 34 CLUSTER A.
FT METAL 38 38 CLUSTER A.
FT METAL 40 40 CLUSTER A.
FT METAL 46 46 CLUSTER A.
FT METAL 50 50 CLUSTER A.
FT METAL 54 54 CLUSTER A.
FT METAL 56 56 CLUSTER A.
FT METAL 57 57 CLUSTER A.
FT VARIANT 1 1 MISSING (IN MT-IIA).
SQ SEQUENCE 58 AA; 6287 MW; EF679CB94975CF0 CRC64;

Query Match 54.9%; Score 28; DB 1; Length 58;
Best Local Similarity 23.5%; Pred. No. 14;
Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2 CXXXXXXCXXXXXXC 18
| | | | |
Db 34 CSSECKTSKECKSKTC 50

RESULT 2

MTL_CALSI STANDARD; PRT; 59 AA.
AC P35949;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN-I (MT-I) (MT-IB/MT-IA).
OS Callinectes sapidus (Blue crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Callinectes.
OX NCBI_TaxID=6763;
RN [1]
RN SEQUENCE.
RX MEDLINE=96033062; PubMed=7487904;
RA Brouwer M., Enghild J., Hoexum-Brouwer T., Thogersen I., Truncali A.;
RT "Primary structure and tissue-specific expression of blue crab
(Callinectes sapidus) metallothionein isoforms.";
RL Biochem. J. 311:617-622(1995).
RN [2]
RN STRUCTURE BY NMR.
RX MEDLINE=95119049; PubMed=7819257;
RA Narula S.S., Brouwer M., Hua Y., Armitage I.M.;
RT "Three-dimensional solution structure of Callinectes sapidus
metallothionein-1 determined by homonuclear and heteronuclear
magnetic resonance spectroscopy";
RL Biochemistry 34:620-631(1995).
CC -1- FUNCTION: BINDS SIX DIVALENT METAL IONS. KNOWN TO BIND COPPER AND
CADMIUM.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR PDB; 1DMC; 07-FEB-95.
DR PDB; 1DME; 07-FEB-95.
DR PDB; 1DMF; 07-FEB-95.
DR InterPro: IPR003019; Metallthion.
DR Pfam: PF00131; metalthio; 1.
DR PRINTS: PR00858; MTCRUSTACEAN
KW Metal-binding; Metal-thiolate cluster; Chelation; Copper; Cadmium;
3D-structure.
FT DOMAIN 1 29 BETA.
FT METAL 30 59 ALPHA.
FT METAL 5 5 CLUSTER B.
FT METAL 6 6 CLUSTER B.
FT METAL 10 10 CLUSTER B.
FT METAL 12 12 CLUSTER B.
FT METAL 17 17 CLUSTER B.
FT METAL 21 21 CLUSTER B.
FT METAL 23 23 CLUSTER B.
FT METAL 26 26 CLUSTER B.
FT METAL 28 28 CLUSTER B.
FT METAL 31 31 CLUSTER A.
FT METAL 34 34 CLUSTER A.
FT METAL 38 38 CLUSTER A.
FT METAL 40 40 CLUSTER A.
FT METAL 46 46 CLUSTER A.
FT METAL 50 50 CLUSTER A.
FT METAL 54 54 CLUSTER A.
FT METAL 56 56 CLUSTER A.
FT METAL 57 57 CLUSTER A.
FT VARIANT 1 1 MISSING (IN MT-IA).
SQ SEQUENCE 59 AA; 6141 MW; 4398BOA9DIA96D34 CRC64;

Query Match 54.9%; Score 28; DB 1; Length 59;
Best Local Similarity 23.5%; Pred. No. 14;

QY 2 CXXXXXXCXXXXXXC 18
| | | | |
Db 34 CTSCKCATKECKSKTC 50

RESULT 3

MTL_SCYSE STANDARD; PRT; 58 AA.
AC P02805;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN-I (MT-I).
OS Scylla setratta (Mud crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Scylla.
OX NCBI_TaxID=6761;
RN [1]
RN SEQUENCE.
RX MEDLINE=82142340; PubMed=7061431;
RA Lerch K., Ammer D., Olafson R.W.;
RT "Crab metallothionein. Primary structures of metallothioneins 1 and
2";
RL J. Biol. Chem. 257:2420-2426(1982).
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS 1 MTS IN MARINE
CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS
OF HEAVY-METAL IONS.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR PIR: A03283; SMKDLS.
DR HSP; P55949; 1DMF.
DR InterPro: IPR003019; Metallthion.
DR InterPro: IPR002045; Metallthion_crust.
DR Pfam: PF00131; metalthio; 1.
DR PRINTS: PR00858; MTCRUSTACEAN.
KW Metal-binding; Metal-thiolate cluster; Chelation.
FT DOMAIN 1 28 BETA.
FT METAL 29 58 ALPHA.
FT METAL 4 4 CLUSTER B.
FT METAL 5 5 CLUSTER B.
FT METAL 9 9 CLUSTER B.
FT METAL 11 11 CLUSTER B.
FT METAL 16 16 CLUSTER B.
FT METAL 20 20 CLUSTER B.
FT METAL 22 22 CLUSTER B.
FT METAL 25 25 CLUSTER B.
FT METAL 27 27 CLUSTER B.
FT METAL 30 30 CLUSTER A.
FT METAL 33 33 CLUSTER A.
FT METAL 37 37 CLUSTER A.
FT METAL 39 39 CLUSTER A.
FT METAL 45 45 CLUSTER A.
FT METAL 49 49 CLUSTER A.
FT METAL 53 53 CLUSTER A.
FT METAL 55 55 CLUSTER A.
FT METAL 56 56 CLUSTER A.
SQ SEQUENCE 58 AA; 6001 MW; CEBA24C590B027B8 CRC64;

Query Match 52.9%; Score 27; DB 1; Length 58;
Best Local Similarity 23.5%; Pred. No. 21;
Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2 CXXXXXXCXXXXXXC 18
| | | | |
Db 33 CSSGCKCANKECKSKTC 49

RESULT 4
NH25_CAEEL

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ID NH25_CASEL STANDARD; PRT; 572 AA.
AC Q19345;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NUCLEAR HORMONE RECEPTOR FAMILY MEMBER NHR-25.
GN NHR-25 OR F11C1.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Palmer S.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ORPHAN NUCLEAR RECEPTOR.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC -----
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CC -----
DR EMBL; Z54270; CAA91028.1; -
DR HSSP; P19793; 2NULL.
DR WormPep; F11C1.6; CE03191.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001628; zf-C4.
DR Pfam; PF00104; hormone_rec. 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; ZnF_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger.
FT DNA_BIND 18 83 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 18 38 C4-TYPE.
FT ZN_FING 54 78 C4-TYPE.
SQ SEQUENCE 572 AA: 64772 MW; D3092AE533092D7A CRC64;

Query Match 52.98; Score 27; DB 1; Length 572;
Best local Similarity 23.58; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 2 CXXXXXXCXXXXXXC 18
Db 54 CSAEANCHVDRTCRKC 70

RESULT 5
LRPI_CHKCK STANDARD; PRT; 4543 AA.
AC P98157;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP)
DE (ALPHA-2-MACROGLOBULIN RECEPTOR) (A2MR).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEHORN; TISSUE=Liver, and Ovary;

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RX MEDLINE-94103212; PubMed-7506255;
RA Nimpf J., Stifani S., Bilous P.T., Schneider W.J.;
RT "The somatic cell-specific low density lipoprotein receptor-related
RT protein of the chicken. Close kinship to mammalian low density
RT lipoprotein receptor gene family members.";
RL J. Biol. Chem. 269:212-219(1994).
CC -1- FUNCTION: INVOLVED IN THE PLASMA CLEARANCE OF CHYLOMICRON REMNANTS
CC AND ACTIVATED ALPHA 2-MACROGLOBULIN, AS WELL AS THE LOCAL
CC METABOLISM OF COMPLEXES BETWEEN PLASMINOGEN ACTIVATORS AND THEIR
CC ENDOGENOUS INHIBITORS. BINDS VITELLOGENIN, CALCIUM AND ALPHA 2-
CC MACROGLOBULIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: IN CLONE JN18, AN ASP IS REPLACED BY
CC SER-GLU-ARG-GLN-ASP DUE TO ALTERNATIVE SPLICING OF EXON3.
CC -1- TISSUE SPECIFICITY: SOMATIC.
CC -1- PTM: CLEAVED INTO A 85 KDA MEMBRANE-SPANNING SUBUNIT (LRP-85) AND
CC A 515 KDA LARGE EXTRACELLULAR DOMAIN (LRP-515) THAT REMAINS NON-
CC COVALENTLY ASSOCIATED.
CC -1- SIMILARITY: CONTAINS 22 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 31 LDL-RECEPTOR CLASS A DOMAINS.
CC -----
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CC -----
DR EMBL; X74904; CAA52870.1; -
DR HSSP; P01130; 1AJJ.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR002172; LDL_recept_A.
DR InterPro; IPR000033; Ldl_recept_rep.
DR Pfam; PF00008; EGF; 16.
DR Pfam; PF00057; ldl_recept_a; 31.
DR Pfam; PF00058; ldl_recept_b; 33.
DR PRINTS; PR00010; EGF_BLOOD.
DR PRINTS; PR00261; LDLRECEPTOR.
DR SMART; SM00179; EGF_CA; 3.
DR SMART; SM00001; EGF_Like; 18.
DR SMART; SM00192; LDLA; 31.
DR SMART; SM00135; LY; 34.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 5.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS01209; LDLRA_1; 27.
DR PROSITE; PS00068; LDLRA_2; 31.
KW Receptor; Transmembrane; Repeat; Endocytosis; Glycoprotein;
KW Signal; Calcium-binding; EGF-like domain; Coated pits;
KW Alternative splicing.
FT SIGNAL 1 21 POTENTIAL..
FT CHAIN 22 4543 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED
FT DOMAIN 22 4419 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 4420 4443 POTENTIAL.
FT DOMAIN 4444 4543 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 27 68 LDL-RECEPTOR CLASS A 1.
FT DOMAIN 72 112 LDL-RECEPTOR CLASS A 2.
FT DOMAIN 113 151 EGF-LIKE 1.
FT DOMAIN 152 191 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 191 222 EGF-LIKE 3.
FT DOMAIN 222 252 EGF-LIKE 4.
FT DOMAIN 252 280 LDL-RECEPTOR CLASS A 3.
FT DOMAIN 280 300 LDL-RECEPTOR CLASS A 4.
FT DOMAIN 300 320 LDL-RECEPTOR CLASS A 5.
FT DOMAIN 320 340 LDL-RECEPTOR CLASS A 6.
FT DOMAIN 340 360 LDL-RECEPTOR CLASS A 7.
FT DOMAIN 360 380 LDL-RECEPTOR CLASS A 8.

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RL EMBO J. 7:4119-4127(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-95203893; PubMed=7534747;
 RA Van Leuven F., Stas L., Halliker C., Lorent K., Umans L., Serneels L.,
 RA Overbergh L., Torrekens S., Moechars D., De Strooper B.,
 RA Van den Berghe H.;
 RT "Structure of the gene (LRPL) coding for the human alpha
 RT 2-macroglobulin receptor lipoprotein receptor-related protein.";
 RL Genomics 24:78-89(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99000832; PubMed=9782078;
 RA Van Leuven F., Stas L., Thiry E., Nellissen B., Miyake Y.;
 RT "Strategy to sequence the 89 exons of the human LRPL gene coding for
 RT the lipoprotein receptor related protein: identification of one
 RT expressed mutation among 48 polymorphisms.";
 RL Genomics 52:138-144(1998).
 RN [4]
 RP PROCESSING.
 RX MEDLINE-90269210; PubMed=2112085;
 RA Herz J., Kowal R.C., Goldstein J.L., Brown M.S.;
 RT "Proteolytic processing of the 600 kd low density lipoprotein
 RT receptor-related protein (LRP) occurs in a trans-Golgi
 RT compartment.";
 RL EMBO J. 9:1769-1776(1990).
 RN [5]
 RP FUNCTION.
 RX MEDLINE-91092405; PubMed=1702392;
 RA Kristensen T., Moestrup S.K., Gilemann J., Bendtsen L., Sand O.,
 RA Sottrup-Jensen L.;
 RT "Evidence that the newly cloned low-density-lipoprotein receptor
 RT related protein (LRP) is the alpha 2-macroglobulin receptor.";
 RL FEBS Lett. 276:151-155(1990).
 RN [6]
 RP STRUCTURE BY NMR OF 1059-1100.
 RX MEDLINE-99253972; PubMed=10318830;
 RA Huang W., Dolmer K., Gettins P.G.W.;
 RT "NMR solution structure of complement-like repeat CR8 from the low
 RT density lipoprotein receptor-related protein.";
 RL J. Biol. Chem. 274:14130-14136(1999).
 CC -!- FUNCTION: INVOLVED IN THE PLASMA CLEARANCE OF CHYLOMICRON REMNANTS
 CC AND ACTIVATION OF COMPLEXES BETWEEN PLASMINOGEN ACTIVATORS AND THEIR
 CC METABOLIC INHIBITORS.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: MOST ABUNDANT IN LIVER, BRAIN AND LUNG.
 CC -!- PTM: CLEAVED INTO A 85 KDA MEMBRANE-SPANNING SUBUNIT (LRP-85) AND
 CC A 515 KDA LARGE EXTRACELLULAR DOMAIN (LRP-515) THAT REMAINS NON-
 CC COVALENTLY ASSOCIATED.
 CC -!- SIMILARITY: CONTAINS 22 EGF-LIKE DOMAINS.
 CC -!- SIMILARITY: CONTAINS 31 LDL-RECEPTOR CLASS A DOMAINS.
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 CC -----
 CC EMBL: X13916; CAA32112.1; -;
 DR EMBL: AF058427; AAC6465.1; -;
 DR PDB: 1CR8; 06-JAN-99.
 DR MIM: 107770; -;
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002172; LDL_recept_A.
 DR InterPro: IPR000033; LDL_recept_rep.
 DR Pfam: PF00008; EGF; 16.
 DR Pfam: PF00057; ldl_recept_a; 31.
 DR Pfam: PF00058; ldl_recept_b; 33.

DR PRINTS: PR00261; LDLRECEPTOR.
 DR SMART; SM00179; EGF_CA; 3.
 DR SMART; SM00001; EGF_LIKE; 19.
 DR SMART; SM00192; LDLa; 31.
 DR SMART; SM00135; LY; 32.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3.
 DR PROSITE; PS00022; EGF_1; 5.
 DR PROSITE; PS01186; EGF_2; 8.
 DR PROSITE; PS01187; EGF_CA; 2.
 DR PROSITE; PS01209; LDLRA_1; 27.
 DR PROSITE; PS00068; LDLRA_2; 31.
 KW Receptor; Transmembrane; Repeat; Endocytosis; Glycoprotein;
 KW Signal; Calcium-binding; EGF-like domain; Coated pits; 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 20 4544
 FT LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED
 FT POTENTIAL.
 FT EXTRACELLULAR (POTENTIAL).
 FT PROTEIN 1.
 FT TRANSMEM
 FT DOMAIN 20 4419
 FT TRANSMEM 4420 4444
 FT DOMAIN 4445 4544
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 25 66
 FT LDL-RECEPTOR CLASS A 1.
 FT DOMAIN 70 110
 FT LDL-RECEPTOR CLASS A 2.
 FT DOMAIN 111 149
 FT EGF-LIKE 1.
 FT DOMAIN 150 189
 FT EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 474 520
 FT EGF-LIKE 3.
 FT DOMAIN 803 843
 FT EGF-LIKE 4.
 FT DOMAIN 852 892
 FT LDL-RECEPTOR CLASS A 3.
 FT DOMAIN 893 933
 FT LDL-RECEPTOR CLASS A 4.
 FT DOMAIN 934 973
 FT LDL-RECEPTOR CLASS A 5.
 FT DOMAIN 974 1013
 FT LDL-RECEPTOR CLASS A 6.
 FT DOMAIN 1013 1053
 FT LDL-RECEPTOR CLASS A 7.
 FT DOMAIN 1060 1099
 FT LDL-RECEPTOR CLASS A 8.
 FT DOMAIN 1102 1142
 FT LDL-RECEPTOR CLASS A 9.
 FT DOMAIN 1143 1182
 FT LDL-RECEPTOR CLASS A 10.
 FT EGF-LIKE 5.
 FT DOMAIN 1183 1222
 FT EGF-LIKE 6.
 FT DOMAIN 1223 1262
 FT EGF-LIKE 7.
 FT DOMAIN 1536 1579
 FT EGF-LIKE 8.
 FT DOMAIN 1846 1887
 FT EGF-LIKE 9.
 FT DOMAIN 2155 2195
 FT EGF-LIKE 10.
 FT DOMAIN 2478 2518
 FT LDL-RECEPTOR CLASS A 11.
 FT DOMAIN 2522 2563
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 FT DOMAIN 2603 2641
 FT LDL-RECEPTOR CLASS A 13.
 FT DOMAIN 2642 2690
 FT LDL-RECEPTOR CLASS A 14.
 FT DOMAIN 2694 2732
 FT LDL-RECEPTOR CLASS A 15.
 FT DOMAIN 2732 2771
 FT LDL-RECEPTOR CLASS A 16.
 FT DOMAIN 2772 2814
 FT LDL-RECEPTOR CLASS A 17.
 FT DOMAIN 2816 2855
 FT LDL-RECEPTOR CLASS A 18.
 FT DOMAIN 2856 2899
 FT LDL-RECEPTOR CLASS A 19.
 FT DOMAIN 2902 2940
 FT LDL-RECEPTOR CLASS A 20.
 FT DOMAIN 2941 2981
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 FT DOMAIN 2982 3022
 FT EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).
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 FT EGF-LIKE 13.
 FT DOMAIN 3063 3102
 FT LDL-RECEPTOR CLASS A 21.
 FT DOMAIN 3103 3142
 FT LDL-RECEPTOR CLASS A 22.
 FT DOMAIN 3143 3182
 FT LDL-RECEPTOR CLASS A 23.
 FT DOMAIN 3183 3222
 FT LDL-RECEPTOR CLASS A 24.
 FT DOMAIN 3223 3262
 FT LDL-RECEPTOR CLASS A 25.
 FT DOMAIN 3263 3302
 FT LDL-RECEPTOR CLASS A 26.
 FT DOMAIN 3303 3342
 FT LDL-RECEPTOR CLASS A 27.
 FT DOMAIN 3343 3382
 FT LDL-RECEPTOR CLASS A 28.
 FT DOMAIN 3383 3422
 FT LDL-RECEPTOR CLASS A 29.
 FT DOMAIN 3423 3462
 FT LDL-RECEPTOR CLASS A 30.
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 FT EGF-LIKE 15.
 FT DOMAIN 3543 3582
 FT EGF-LIKE 16.
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 FT EGF-LIKE 17.
 FT DOMAIN 3623 3662
 FT EGF-LIKE 18.
 FT DOMAIN 3663 3702
 FT EGF-LIKE 19.
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 FT EGF-LIKE 3

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FT SITE 4473 4473 PROCESSING (POTENTIAL).
FT DOMAIN 4502 4507 CRITICAL FOR ENDOCYTOSIS (POTENTIAL).
FT DISULFID 27 40 ENDOCYTOSIS SIGNAL (POTENTIAL).
FT DISULFID 34 53 BY SIMILARITY.
FT DISULFID 47 64 BY SIMILARITY.
FT DISULFID 72 85 BY SIMILARITY.
FT DISULFID 79 98 BY SIMILARITY.
FT DISULFID 92 108 BY SIMILARITY.
FT DISULFID 115 124 BY SIMILARITY.
FT DISULFID 120 133 BY SIMILARITY.
FT DISULFID 135 148 BY SIMILARITY.
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FT DISULFID 160 173 BY SIMILARITY.
FT DISULFID 175 188 BY SIMILARITY.
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FT DISULFID 984 1002 BY SIMILARITY.

Query Match 52.9%; Score 27; DB 1; Length 4544;
Best Local Similarity 23.5%; Pred. No. 48;
Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2 CXXXXXXCXXXXXXC 18
DB 2980 CADVDCSTTTPCQRC 2996

RESULT 7
MT2_SCYSE STANDARD; PRT; 57 AA.
AC P02806;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN-II (MT-II).
OS Scylla serrata (Mud crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchyura; Portunoidae; Portunidae; Scylla.
OX NCBI_TaxID=6761;
RN [1]
RP SEQUENCE.
RX MEDLINE=82142340; PubMed=7061431;
RA Lerch K., Ammer D., Olafson R.W.;
RT "Crab metallothionein. Primary structures of metallothioneins 1 and 2.";
RL J. Biol. Chem. 257:2420-2426(1982).
CC -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN MARINE
CC CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS
CC OF HEAVY-METAL IONS.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
CC PIR: A03284; SWKD25.
DR HSP: P55949; IDMF.
DR InterPro: IPR003019; Metallthion.
DR InterPro: IPR002045; Metallthion_crust.
DR Pfam: PF00131; metalthio; 1.
DR PRINTS: PR00858; MTCRUSTACEAN.
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KW Metal-binding: Metal-thiolate cluster; Chelation.
FT DOMAIN 1 28 BETA.
FT DOMAIN 29 57 ALPHA.
FT METAL 4 4 CLUSTER B.
FT METAL 5 5 CLUSTER B.
FT METAL 9 9 CLUSTER B.
FT METAL 11 11 CLUSTER B.
FT METAL 16 16 CLUSTER B.
FT METAL 20 20 CLUSTER B.
FT METAL 22 22 CLUSTER B.
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FT METAL 39 39 CLUSTER A.
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FT METAL 49 49 CLUSTER A.
FT METAL 53 53 CLUSTER A.
FT METAL 55 55 CLUSTER A.
FT METAL 56 56 CLUSTER A.
SQ SEQUENCE 57 AA; 6109 MW; 8C2B3F6A6BAA3611 CRC64;

Query Match 51.0%; Score 26; DB 1; Length 57;
Best Local Similarity 23.5%; Pred. No. 33;
Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2 CXXXXXXCXXXXXXC 18
DB 33 CSSGCKCANKEDCRKTC 49

RESULT 8
MT1_HOMAM STANDARD; PRT; 58 AA.
AC P29499;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN-1 (CUMT-1).
OS Homarus americanus (American lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
OX NCBI_TaxID=6706;
RN [1]
RP SEQUENCE.
RC TISSUE=Hepatopancreas;
RX MEDLINE=89215793; PubMed=2709004;
RA Brouwer M., Winge D.R., Gray W.R.;
RT "Structural and functional diversity of copper-metalllothioneins from the American lobster Homarus americanus.";
RL J. Inorg. Biochem. 35:289-303(1989).
RN [2]
RP STRUCTURE BY NMR.
RX MEDLINE=94318629; PubMed=8043573;
RA Zhu Z., Derose E.F., Mullen G.P., Petering D.H., Shaw C.F. III;
RT "Sequential proton resonance assignments and metal cluster topology of lobster metallothionein-1.";
RL Biochemistry 33:8858-8865(1994).
CC -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS. THE DIFFERENT FORMS OF
CC LOBSTER METALLOTHIONEINS MAY HAVE DIFFERENT BIOLOGICAL FUNCTIONS.
CC CLASS I MTS IN MARINE CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION
CC OF ELEVATED LEVELS OF HEAVY-METAL IONS. BINDS 6 METAL IONS. KNOWN
CC TO BIND CADMIUM.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
CC PIR: A37039; A37039.
DR HSP: P55949; IDMF.
DR InterPro: IPR003019; Metallthion.
DR InterPro: IPR002045; Metallthion_crust.
DR Pfam: PF00131; metalthio; 1.
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DR PRINTS: PR00858; MTCRUSTACEAN.
KW Metal-binding; Metal-thiolate cluster; Chelation; Copper; Cadmium.
FT DOMAIN 1 28 BETA.
FT METAL 29 58 ALPHA.
FT METAL 4 4 CLUSTER B.
FT METAL 5 5 CLUSTER B.
FT METAL 9 9 CLUSTER B.
FT METAL 11 11 CLUSTER B.
FT METAL 16 16 CLUSTER B.
FT METAL 20 20 CLUSTER B.
FT METAL 22 22 CLUSTER B.
FT METAL 25 25 CLUSTER B.
FT METAL 27 27 CLUSTER B.
FT METAL 30 30 CLUSTER A.
FT METAL 33 33 CLUSTER A.
FT METAL 37 37 CLUSTER A.
FT METAL 39 39 CLUSTER A.
FT METAL 45 45 CLUSTER A.
FT METAL 49 49 CLUSTER A.
FT METAL 53 53 CLUSTER A.
FT METAL 55 55 CLUSTER A.
FT METAL 56 56 CLUSTER A.
SQ SEQUENCE 58 AA; 5975 MW; 176ABAAF60A32F96 CRC64;

Query Match 51.0%; Score 26; DB 1; Length 58;
Best Local Similarity 23.5%; Pred. No. 33;
Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 2 CXXXXXXCXXXXXXC 18
Db 33 CTSGCKCPKDECAKTC 49

RESULT 9
- MT_ASTFL ID MT_ASTFL STANDARD; PRT; 58 AA.
AC P55951;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN (MT).
OS Astacus fluviatilis (Broad-fingered crayfish) (Astacus astacus).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacidea; Astacidae; Astacus.
OX NCBI_TaxID=6715;
RN [1]
RP SEQUENCE.
RC TISSUE=Midgut;
RX MEDLINE=97079279; PubMed=8921011;
RA Pedersen S.N., Pedersen K.L., Hoejrup P., Depledge M.H., Knudsen J.;
RT "Primary structures of decapod crustacean metallothioneins with special emphasis on freshwater and semi-terrestrial species.";
RL Biochem. J. 319:999-1003(1996).
CC -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS OF HEAVY-METAL IONS.
CC -!- INDUCTION: BY CADMIUM.
CC -!- MASS SPECTROMETRY: MW=5910.8; METHOD=NALDI.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR InterPro; IPR003019; Metallthion.
DR Pfam; PF00131; metalthio; 1.
DR PRINTS; PR00858; MTCRUSTACEAN.
KW Metal-binding; Metal-thiolate cluster; Chelation; Cadmium.
FT DOMAIN 1 29 BETA.
FT METAL 30 58 ALPHA.
FT METAL 5 5 CLUSTER B.
FT METAL 6 6 CLUSTER B.
FT METAL 10 10 CLUSTER B.

FT METAL 12 12 CLUSTER B.
FT METAL 17 17 CLUSTER B.
FT METAL 21 21 CLUSTER B.
FT METAL 23 23 CLUSTER B.
FT METAL 26 26 CLUSTER B.
FT METAL 28 28 CLUSTER B.
FT METAL 31 31 CLUSTER A.
FT METAL 34 34 CLUSTER A.
FT METAL 38 38 CLUSTER A.
FT METAL 40 40 CLUSTER A.
FT METAL 46 46 CLUSTER A.
FT METAL 50 50 CLUSTER A.
FT METAL 54 54 CLUSTER A.
FT METAL 56 56 CLUSTER A.
FT METAL 57 57 CLUSTER A.
FT VARIANT 1 1 MISSING (IN VARIANT ISOLATED IN LOW CADMIUM CONCENTRATION).
SQ SEQUENCE 58 AA; 5911 MW; 576365B3E5C7122 CRC64;

Query Match 51.0%; Score 26; DB 1; Length 58;
Best Local Similarity 23.5%; Pred. No. 33;
Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 2 CXXXXXXCXXXXXXC 18
Db 34 CTSGCKCPKDECAKTC 50

RESULT 10
- MT_CARMA ID MT_CARMA STANDARD; PRT; 58 AA.
AC P55948;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE METALLOTHIONEIN (MT).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoida; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Midgut;
RX MEDLINE=94153337; PubMed=8110201;
RA Pedersen K.L., Pedersen S.N., Hoejrup P., Andersen J.S., Roepstorff P., Knudsen J., Depledge M.H.;
RT "Purification and characterization of a cadmium-induced metallothionein from the shore crab Carcinus maenas (L.).";
RL Biochem. J. 297:609-614(1994).
CC -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN MARINE CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS OF HEAVY-METAL IONS.
CC -!- INDUCTION: BY CADMIUM.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR InterPro; IPR003019; Metallthion.
DR HSSP; P55949; 1DMD.
DR Pfam; PF00131; metalthio; 1.
DR InterPro; IPR002045; Metallthion_crust.
DR PRINTS; PR00858; MTCRUSTACEAN.
KW Metal-binding; Metal-thiolate cluster; Chelation; Cadmium.
FT DOMAIN 1 29 BETA.
FT METAL 30 58 ALPHA.
FT METAL 5 5 CLUSTER B.
FT METAL 6 6 CLUSTER B.
FT METAL 10 10 CLUSTER B.
FT METAL 12 12 CLUSTER B.
FT METAL 17 17 CLUSTER B.
FT METAL 21 21 CLUSTER B.
FT METAL 23 23 CLUSTER B.
FT METAL 26 26 CLUSTER B.

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FT METAL 28 31 34 38 40 46 50 54 56 57 1
FT METAL 31 34 38 40 46 50 54 56 57 1
FT METAL 34 38 40 46 50 54 56 57 1
FT METAL 38 40 46 50 54 56 57 1
FT METAL 40 46 50 54 56 57 1
FT METAL 46 50 54 56 57 1
FT METAL 50 54 56 57 1
FT METAL 54 56 57 1
FT METAL 56 57 1
FT METAL 57 1
FT VARIANT 1
FT MISSING (IN VARIANT ISOLATED IN LOW
FT CADMIUM CONCENTRATION).
SQ SEQUENCE 58 AA; 6133 MW; 0167CDA2E9C9731D CRC64;

Query Match 51.0%; Score 26; DB 1; Length 58;
Best Local Similarity 23.5%; Pred. No. 33;
Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2 CXXXXXXCXXXXXXC 18
DB 34 CSSGCKTTKEDCKTC 50

RESULT 11
MT_POTPO STANDARD; PRT; 58 AA.
AC P55952;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN (MT).
OS Potamon potamos.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchyura; Potamoidea; Potamidae; Potamon.
OX NCBI_TaxID=59185;
RN [1]
RP SEQUENCE.
RC TISSUE=Midgut;
RX MEDLINE=97079279; PubMed=8921011;
RA Pedersen S.N., Pedersen K.L., Hoeirup P., Knudsen J.;
RT "Primary structures of decapod crustacean metallothioneins with
RT special emphasis on freshwater and semi-terrestrial species.";
RL Biochem. J. 319:999-1003(1996).
CC -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN CRUSTACEA
CC ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS OF HEAVY-
CC METAL IONS.
CC -!- INDUCTION: BY CADMIUM.
CC -!- MASS SPECTROMETRY: MW=6156.8; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR HSP; P55949; 1DMD.
DR InterPro; IPR003019; Metallthion.
DR Pfam; PF00131; metalthio; 1.
DR PRINTS; PR00858; MTCRUSTACEAN.
KW Metal-binding; Metal-thiolate cluster; Chelation; Cadmium.
FT DOMAIN 1 29
FT METAL 30 58 ALPHA.
FT METAL 4 4 CLUSTER B.
FT METAL 5 5 CLUSTER B.
FT METAL 10 10 CLUSTER B.
FT METAL 12 12 CLUSTER B.
FT METAL 17 17 CLUSTER B.
FT METAL 21 21 CLUSTER B.
FT METAL 23 23 CLUSTER B.
FT METAL 26 26 CLUSTER B.
FT METAL 28 28 CLUSTER B.
FT METAL 31 31 CLUSTER A.
FT METAL 34 34 CLUSTER A.
FT METAL 38 38 CLUSTER A.
FT METAL 40 40 CLUSTER A.

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FT METAL 46 46 CLUSTER A.
FT METAL 50 50 CLUSTER A.
FT METAL 54 54 CLUSTER A.
FT METAL 56 56 CLUSTER A.
FT METAL 57 57 CLUSTER A.
SQ SEQUENCE 58 AA; 6157 MW; DCB71F9AB4DF779C CRC64;

Query Match 51.0%; Score 26; DB 1; Length 58;
Best Local Similarity 23.5%; Pred. No. 33;
Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2 CXXXXXXCXXXXXXC 18
DB 34 CTSECECKSKKECAKNC 50

RESULT 12
THBL_THETS STANDARD; PRT; 67 AA.
AC P82354;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE THEROMIN (THROMBIN INHIBITOR).
OS Theromyzon tessulatum (Leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
OX NCBI_TaxID=13286;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Head;
RX MEDLINE=20469422; PubMed=10837466;
RA Salzet M., Chopin V., Baert J.-L., Matias I., Malecha J.;
RT "Theromin, a novel leech thrombin inhibitor.";
RL J. Biol. Chem. 275:30774-30780(2000).
CC -!- FUNCTION: POTENT THROMBIN-SPECIFIC INHIBITOR.
CC -!- SUBUNIT: HOMODIMER.
CC -!- PTM: EIGHT DISULFIDE BONDS ARE PRESENT.
CC -!- MASS SPECTROMETRY: MW=14491; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE ANTISTASIN FAMILY.
KW Serine protease inhibitor.
FT ACT_SITE 36 37 REACTIVE BOND (BY SIMILARITY).
SQ SEQUENCE 67 AA; 7257 MW; 1956FEE93A57B4FA CRC64;

Query Match 51.0%; Score 26; DB 1; Length 67;
Best Local Similarity 23.5%; Pred. No. 34;
Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2 CXXXXXXCXXXXXXC 18
DB 48 CTCNTRCSADECNPRC 64

RESULT 13
TNRL_HUMAN STANDARD; PRT; 455 AA.
AC P19438;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR
DE BINDING PROTEIN 1) (TNFRI) (P60) (TNF-RI) (P55) (CD120A).
GN TNFRSF1A OR TNFRI OR TNFAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90235285; PubMed=2158863;

```

RA Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,
RA Getanaga T., Granger G.A., Lentz R., Raab H., Kohn W.J., Geddel D.V.;
RT "Molecular cloning and expression of a receptor for human tumor
RL necrosis factor.";
RL Cell 61:361-370(1990).
RN [2]
RN SEQUENCE FROM N.A.
RP MEDLINE-90235284; PubMed-2159862;
RX Loelscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,
RA Tabuchi H., Lesslauer W.;
RT "Molecular cloning and expression of the human 55 kd tumor necrosis
RT factor receptor.";
RL Cell 61:351-359(1990).
RN [3]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.
RX MEDLINE-91006021; PubMed-1698610;
RA Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zhang R.,
RA Aderka D., Holtmann H., Wallach D.;
RT "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
RT for the type I TNF-R, cloned using amino acid sequence data of its
RT soluble form, encodes both the cell surface and a soluble form of the
RT receptor.";
RL Embo J. 9:3269-3278(1990).
RN [4]
RN SEQUENCE FROM N.A.
RX MEDLINE-91090841; PubMed-1702293;
RA Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
RA Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT "Molecular cloning and expression of human and rat tumor necrosis
RT factor receptor chain (p60) and its soluble derivative, tumor
RT necrosis factor-binding protein.";
RL DNA Cell Biol. 9:705-715(1990).
RN [5]
RN SEQUENCE FROM N.A.
RX MEDLINE-91017509; PubMed-2170974;
RA Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.;
RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and
RT expression of recombinant soluble TNF-binding protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
RN [6]
RN SEQUENCE FROM N.A.
RX MEDLINE-92250049; PubMed-1315717;
RA Fuchs P., Strehl S., Dworzak M., Himmler A., Ambros P.F.;
RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
RT localization to chromosome 12p13.";
RL Genomics 13:219-224(1992).
RN [7]
RN SEQUENCE OF 41-45.
RX MEDLINE-90110215; PubMed-2153136;
RA Engelmann H., Novick D., Wallach D.;
RT "Two tumor necrosis factor-binding proteins purified from human
RT urine. Evidence for immunological cross-reactivity with cell surface
RT tumor necrosis factor receptors.";
RL J. Biol. Chem. 265:1531-1536(1990).
RN [8]
RN X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNF.
RX MEDLINE-93258609; PubMed-8387891;
RA Banner D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J.,
RA Broger C., Loetscher H., Lesslauer W.;
RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
RT beta complex: implications for TNF receptor activation.";
RL Cell 73:431-445(1993).
RN [9]
RN X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
RX MEDLINE-97094982; PubMed-8939750;
RA Naismith J.H., Devine T.Q., Khono H., Sprang S.R.;
RT "Structures of the extracellular domain of the type I tumor necrosis
RT factor receptor.";
RL Structure 4:1251-1262(1996).
CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)

CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC PROTEASES) MEDIATING APOPTOSIS. CONTRIBUTES TO THE INDUCTION OF
CC NONCYTOLIC TNF EFFECTS INCLUDING ANTI-VIRAL STATE AND ACTIVATION
CC OF THE ACID SPHINGOMYELINASE.
CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC NF-KAPPA B SIGNALING.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO
CC THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH
CC NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD120a entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120a.htm".
CC -----
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CC -----
DR EMBL; X55313; AAA39021.1; -;
DR EMBL; M33294; AAA03210.1; -;
DR EMBL; M58286; AAA36753.1; -;
DR EMBL; M63121; AAA36754.1; -;
DR EMBL; M75866; AAA61201.1; -;
DR EMBL; M75864; AAA61201.1; JOINED.
DR EMBL; M75865; AAA61201.1; JOINED.
DR EMBL; M60275; AAA36756.1; -;
DR EMBL; A21522; CAA01558.1; -;
DR PIR; A34899; GQH011.
DR PIR; A35010; A35010.
DR PIR; S12057; S12057.
DR PIR; A38208; A38208.
DR PDB; 1NCF; 07-DEC-95.
DR PDB; 1EXT; 11-JAN-97.
DR MM; 191190; -;
DR InterPro; IPR000488; Death..
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis;
KW 3D-structure.
FT SIGNAL 1 21
FT CHAIN 22 455 TUMOR NECROSIS FACTOR RECEPTOR 1.
FT CHAIN 41 291 TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
FT DOMAIN 22 211 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 212 234 POTENTIAL.
FT DOMAIN 235 455 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 43 196 4 X TNFR-CYS.
FT REPEAT 43 82 TNFR-CYS 1.
FT REPEAT 83 125 TNFR-CYS 2.
FT REPEAT 126 166 TNFR-CYS 3.
FT REPEAT 167 196 TNFR-CYS 4.
FT DOMAIN 338 348 N-SMASE ACTIVATION DOMAIN (NSD).
FT DOMAIN 356 441 DEATH.
FT DISULFID 44 58

QY 2 CXXXXXXCXXXXXXC 18
| | | | |
Db 252 CVDINECDASNOCAQC 268

RESULT 15
FBL3_RAT
ID FBL3_RAT STANDARD; PRT: 493 AA.
AC Q35568;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR
DE (FIBULIN-3) (FIBL-3) (16 PROTEIN).
GN EFEMP1 OR FBLN3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=97415782; PubMed=9268694;
RA Ozaki T., Kondo K., Nakamura Y., Ichimiya S., Nakagawara A.,
RA Sakiyama S.;
RT "Interaction of DA41, a DAN-binding protein, with the epidermal growth
factor-like protein, S(1-5).";
RL Biochem Biophys Res Commun. 237:245-250(1997).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL; D89730; BAA22265.1; -
DR HSP; P35555; IEMO.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_CA.
DR Pfam: PF00008; EGF; 4.
DR SMART; SM00179; EGF_CA; 4.
DR SMART; SM00001; EGF_Like; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS01187; EGF_CA; 6.
KW Repeat; EGF-like domain; Calcium-binding; Glycoprotein; Signal.
FT SIGNAL 1 17
FT CHAIN 18 493
FT FT
FT DOMAIN 26 71
FT DOMAIN 173 213
FT DOMAIN 214 253
FT DOMAIN 254 293
FT DOMAIN 294 333
FT DOMAIN 334 378
FT DISULFID 177 190
FT DISULFID 184 199
FT DISULFID 201 212
FT DISULFID 218 228
FT DISULFID 224 237
FT DISULFID 239 252
FT DISULFID 258 268
FT DISULFID 264 277
FT DISULFID 279 292
FT DISULFID 298 309
FT DISULFID 305 318
FT DISULFID 320 332

FT DISULFID 338 350 BY SIMILARITY.
FT DISULFID 344 359 BY SIMILARITY.
FT DISULFID 365 377 BY SIMILARITY.
SQ SEQUENCE 493 AA; 54596 MW; 22DAFD70BACF1CA5 CRC64;

Query Match 51.0%; Score 26; DB 1; Length 493;
Best Local Similarity 23.5%; Pred. No. 50;
Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2 CXXXXXXCXXXXXXC 18
| | | | |
Db 252 CVDINECDASNOCAQC 268

Search completed: February 13, 2002, 10:11:04
Job time: 112 sec
